

A natural polymorphism in Zika virus NS2A protein responsible of virulence in mice

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Supplementary Table 1. Differences between University of Rochester (UR) ZIKV-Paraiba and ZIKV-Paraiba reference sequence in Genbank (accession number **KX280026). Nucleotides differences with more than 50% of frequency that result in amino acid changes are shown in italic. ^aOnly quasiespecies with more than 10% of frequency are shown. Rows highlighted in grey indicate amino acid changes. ^bAmino acid changes in ZIKV proteins.**

Nucleotide sequence			Amino acid sequence				
Nucleotide position	Reference sequence	UR sequence ^a	Polypeptide position	Protein position ^b	Reference sequence	UR sequence	Protein
535	<i>A</i>	<i>A 33%</i>	143	21	<i>E</i>	<i>E 33%</i>	<i>prM</i>
		<i>G 67%</i>				<i>G 67%</i>	
693	<i>A</i>	<i>G 100%</i>	196	74	<i>T</i>	<i>A 100%</i>	<i>prM</i>
798	<i>T</i>	<i>C 100%</i>	231	109	<i>S</i>	<i>P 100%</i>	<i>prM</i>
1,646	<i>A</i>	<i>A 81%</i>	-	-	-	-	<i>E</i>
		<i>G 19%</i>				-	
2,178	<i>C</i>	<i>C 65%</i>	691	401	<i>H</i>	<i>H 65%</i>	<i>E</i>
		<i>T 35%</i>				<i>Y 35%</i>	
2,960	<i>T</i>	<i>T 86%</i>	-	-	-	-	<i>NS1</i>
		<i>C 14%</i>				-	
3,400	<i>G</i>	<i>G 88%</i>	1,098	304	<i>S</i>	<i>S 88%</i>	<i>NS1</i>
		<i>A 12%</i>				<i>N 12%</i>	
3,828	<i>T</i>	<i>T 63%</i>	1,241	95	<i>F</i>	<i>F 63%</i>	<i>NS2A</i>

		C 37%				L 37%	
3,895	C	C 47%	1,263	117	A	A 47%	NS2A
		T 53%				V 53%	
4,667	C	C 71%	-	-	-	-	NS3
		T 29%					
5,614	T	T 27%	1,836	334	M	M 27%	NS3
		C 63%				T 63%	
6,373	A	G 100%	2,089	587	K	R 100%	NS3
6,724	C	C 83%	2,206	86	T	T 83%	NS4A
		T 17%				I 17%	
7,136	T	T 68%	-	-	-	-	NS4B